

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Aug 08 11:54:07 EDT 2007

=====

Application No: 10780638

Version No: 2.0

Input Set:**Output Set:****Started:** 2007-08-07 17:13:50.435**Finished:** 2007-08-07 17:13:52.249**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 814 ms**Total Warnings:** 33**Total Errors:** 0**No. of SeqIDs Defined:** 33**Actual SeqID Count:** 33

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-08-07 17:13:50.435
Finished: 2007-08-07 17:13:52.249
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 814 ms
Total Warnings: 33
Total Errors: 0
No. of SeqIDs Defined: 33
Actual SeqID Count: 33

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research Organization

<120> Efficient gene silencing in plants using short dsRNA sequences

<130> BCS-03-2001

<140> 10780638

<141> 2004-02-19

<150> US 60/447,711

<151> 2003-02-19

<160> 33

<170> PatentIn version 3.3

<210> 1

<211> 341

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the 7SL-2 gene of Arabidopsis thaliana var. Landsberg erecta

<220>

<221> misc_feature

<222> (1)..(6)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (7)..(322)

<223> PolIII promoter region

<220>

<221> misc_feature

<222> (323)..(328)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (329)..(335)

<223> poly T nucleotide stretch

<220>

<221> misc_feature

<222> (336)..(341)

<223> XhoI restriction site

<400> 1

ctcgagatgt tgttggtacc agaaagtaaa taaatgttca atctctgatg ttctcaagta 60

agtgagtttt attgggaata atattaactc atgttcttct gcatttgatt cctttgccgc 120

tctcttcttc tatcttaaatt ctgtgtatac tatttcacta ttgggctttt tattagtcta 180
 taatgggact caaaataagg ctttggccca catcaaaaag ataagtcaca aatcaaaaact 240
 aaattcagag tcttttctcc cacatcggtc actgtactca ttttgtgttt gtttatatat 300
 tacacgaacc gatctttgtt acgtcgactt tttttctega g 341

<210> 2

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the 7SL-2 gene of Arabidopsis thaliana var. Landsberg erecta including 86 bases downstream of the transcription initiation site.

<220>

<221> misc_feature

<222> (1)..(6)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (7)..(408)

<223> PolIII promoter region.

<220>

<221> misc_feature

<222> (409)..(414)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (415)..(423)

<223> poly T stretch

<220>

<221> misc_feature

<222> (424)..(429)

<223> XhoI restriction site

<400> 2

ctcgagatgt tgttggtacc agaaagtaaa taaatgttca atctctgatg ttctcaagta 60
 agtgagtttt attgggaata atattaactt atgttcttct tgcatttgat ttctttgccg 120
 ctctcttctt ctatcttaaa tctgtgtata ctatttcact attgggcttt ttattagtct 180
 ataatgggac tcaaaataag gctttggccc acatcaaaaa gataagtcac aaatcaaaac 240
 taaattcaga gtcttttctc ccacatcggt cactgtactc ttttgtgttt gtttatatat 300

tacacgaacc gatcttttggc acgtcgagct aagtaacatg agcttgtaac ccatgtgggg 360

acattaagat ggtggaacac tggctcgggt ccacgggccg gttctgttgt cgactttttt 420

tttctcgag 429

<210> 3

<211> 334

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA of Arabidopsis thaliana var. Landsberg erecta

<220>

<221> misc_feature

<222> (1)..(6)

<223> EcoRI restriction site

<220>

<221> misc_feature

<222> (7)..(313)

<223> Pol III promoter region

<220>

<221> misc_feature

<222> (314)..(319)

<223> PvuI restriction site

<220>

<221> misc_feature

<222> (320)..(328)

<223> poly T stretch

<220>

<221> misc_feature

<222> (329)..(334)

<223> EcoRI restriction site

<400> 3

gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga 60

agatctgttt tggctatgtt ggacgaaaca agtgaacttt taggatcaac ttcagtttat 120

atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat 180

cgtccataga ttcactaata cccatgccca gtacccatgt atgcgtttca tataagctcc 240

taatttctcc cacatcgctc aaatctaaac aaatcttggt gtatatataa cactgaggga 300

gcaacattgg tcacgatcgt ttttttttga attc 334

<210> 4

<211> 467
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the promoter of the U3 snRNA gene of Arabidopsis thaliana var. Landsberg erecta including 136 bases downstream of the transcription initiation site.

<220>
 <221> misc_feature
 <222> (1)..(6)
 <223> EcoRI restriction site

<220>
 <221> misc_feature
 <222> (7)..(446)
 <223> Pol III promoter region

<220>
 <221> misc_feature
 <222> (447)..(452)
 <223> XhoI restriction site

<220>
 <221> misc_feature
 <222> (453)..(461)
 <223> poly T stretch

<220>
 <221> misc_feature
 <222> (462)..(467)
 <223> EcoRI restriction site

<400> 4
 gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga 60
 agatctgttt tggctatggt ggacgaaaca agtgaacttt taggatcaac ttcagtttat 120
 atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat 180
 cgtccataga ttcactaata cccatgccca gtacccatgt atgcgtttca tataagctcc 240
 taatttctcc cacatcgctc aaatctaaac aaatcttggt gtatatataa cactgaggga 300
 gcaacattgg tcacgacctt acttgaacag gatctgttct ataggctcgt acctctgttt 360
 ccttgatttc tcaagagaca ggcccttaac cctggttgat gaaccatgac cgtgcggcta 420
 ggcgtgatt gacggctacg atcgctctcg agtttttttt tgaattc 467

<210> 5
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>

<223> sequence of the promoter of the U6-26 snRNA gene of *Arabidopsis thaliana* var. *Landsberg erecta* including 3 bases downstream of the transcription initiation site, followed by a unique restriction site in front of an oligo dT stretch

<220>

<221> misc_feature

<222> (1)..(6)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (7)..(436)

<223> Pol III promoter region

<220>

<221> misc_feature

<222> (437)..(442)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (443)..(450)

<223> poly T stretch

<220>

<221> misc_feature

<222> (451)..(456)

<223> Sac I restriction site

<400> 5

ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaataca tcatttcttc	60
ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt	120
cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg	180
tttcatagtt tgtcccagga ttagaatgat taggcacga accttcaaga atttgattga	240
ataaaacatc ttcattctta agatatgaag ataattctca aaaggccctt gggaatctga	300
aagaagagaa gcaggcccat ttatatggga aagaacaata gtattttctta tataggccca	360
tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag	420
tttatataca gctagagtcg actttttttt gagctc	456

<210> 6

<211> 488

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U6-26 snRNA gene of Arabidopsis thaliana var. Landsberg erecta including 20 bases downstream of the transcription initiation site, followed by a unique restriction site in front of an oligo dT stretch

<220>

<221> misc_feature

<222> (1)..(6)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (7)..(468)

<223> Pol III promoter region

<220>

<221> misc_feature

<222> (469)..(474)

<223> PvuI restriction site

<220>

<221> misc_feature

<222> (475)..(482)

<223> Poly T stretch

<220>

<221> misc_feature

<222> (483)..(488)

<223> XhoI restriction site

<400> 6

ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaataca tcatttcttc	60
ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt	120
cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg	180
tttcatagtt tgtcccagga ttagaatgat taggcacga accttcaaga atttgattga	240
ataaaacatc ttcattctta agatatgaag ataattctca aaaggccctt gggaatctga	300
aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggcca	360
tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag	420
tttatataca gctagagtcg aagtagtgat tgtcccttcg gggacatccg atcgtttttt	480
ttctcgag	488

<210> 7

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA of rice (*Oryza sativa* Indica IR36)

<220>

<221> misc_feature

<222> (1)..(6)

<223> EcoRI restriction site

<220>

<221> misc_feature

<222> (7)..(384)

<223> Pol III promoter region

<220>

<221> misc_feature

<222> (385)..(390)

<223> PvuI restriction site

<220>

<221> misc_feature

<222> (391)..(399)

<223> poly T stretch

<220>

<221> misc_feature

<222> (400)..(405)

<223> EcoRI restriction site

<400> 7

gaattcaagg gatctttaaa catacgaaca gatcacttaa agttcttctg aagcaactta 60

aagttatcag gcatgcatgg atcttgagg aatcagatgt gcagtcagg accatagcac 120

aggacaggcg tcttctactg gtgctaccag caaatgctgg aagccgggaa cactgggtac 180

gttggaacc acgtgatgtg gagtaagata aactgtagga gaaaagcatt tcgtagtggg 240

ccatgaagcc tttcaggaca tgtattgcag tatgggccgg cccattacgc aattggacga 300

caacaaagac tagtattagt accacctcgg ctatccacat agatcaaagc tggtttaaaa 360

gagttgtgca gatgatccgt ggcacgatcg ttttttttg aattc 405

<210> 8

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA of tomato (a garden variety with small gourd-shaped yellow fruit)

<220>

<221> misc_feature

<222> (1)..(6)
<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (7)..(421)
<223> Pol III promoter region

<220>
<221> misc_feature
<222> (422)..(427)
<223> PvuI restriction site

<220>
<221> misc_feature
<222> (428)..(436)
<223> Poly T stretch

<220>
<221> misc_feature
<222> (437)..(442)
<223> EcoRI restriction site

<400> 8
gaattctgag agcattgtgt ggcgttctc tgaattactt actgtcactt tgattggagc 60

cattattttc agactctact gaagattgaa ttgaatgaga aactatgaaa ctttacaagt 120

gaattattat ggagttcatg gcaactgcta tggagttttt cctactggga attggaacgg 180

tttctacgaa attaactgtc cacacgttaa aaatataaat taatgcgtaa ttgttatttt 240

ttctataaca aataaaaaaac tgaaatacga cataaatttt attactttaa ttgcacttta 300

gccttagaga tattgcgttg tagtcggcgt aggtgtgtca ggggccaata tattgttccc 360

acatcggcag tgcagcacat aaactctagc gttataagaa tctatccact atcaacggtc 420

acgatcgttt ttttttgaat tc 442

<210> 9
<211> 295
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 94bp for silencing
expression of the GUS gene (GUShp94)

<220>
<221> misc_feature
<222> (1)..(6)
<223> SalI restriction site

<220>

<221> misc_feature
<222> (6)..(11)
<223> PvuI restriction site

<220>
<221> misc_feature
<222> (12)..(100)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (101)..(195)
<223> spacer sequence

<220>
<221> misc_feature
<222> (190)..(195)
<223> BamHI restriction site

<220>
<221> misc_feature
<222> (196)..(284)
<223> GUS sequence (antisense)

<220>
<221> misc_feature
<222> (285)..(290)
<223> PvuI restriction site

<220>
<221> misc_feature
<222> (290)..(295)
<223> SalI restriction site

<400> 9
gtcgacgatc gcagcgtaat gctctacacc acgccgaaca cctgggtgga cgatatcacc 60

gtggtgacgc atgtcgcgca agactgtaac cacgcgtctg ttgactggca ggtggtggcc 120

aatggtgatg tcagcgttga actgcgtgat gcgcatcaac aggtggttgc aactggacaa 180

ggcactagcg ggatccagac gcgtgggttac agtcttgccg gacatgcgtc accacggtga 240

tategtccac ccaggtgttc ggcgtggtgt agagcattac gctgcgatcg tcgac 295

<210> 10
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 41 bp for silencing
expression of the GUS gene (GUShp41)

<220>

<221> misc_feature
<222> (1)..(6)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (7)..(42)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (43)..(51)
<223> spacer sequence

<220>
<221> misc_feature
<222> (52)..(87)
<223> GUS sequence (antisense)

<220>
<221> misc_feature
<222> (88)..(93)
<223> Sal I restriction site

<400> 10
gtcgactggg cagatgaaca tggcatcgtg gtgattgatg aatgcgagaa cttcatcaat 60

caccacgatg ccatgttcat ctgccagtc gac 93

<210> 11
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
expression of the GUS gene (GUShp21)

<220>
<221> misc_feature
<222> (1)..(6)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (7)..(22)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (23)..(28)
<223> spacer sequence

<220>
<221> misc_feature

<222> (29)..(44)
 <223> GUS sequence (antisense)

<220>
 <221> misc_feature
 <222> (45)..(50)
 <223> Sal I restriction site

<400> 11
 gtcgactggg cagatgaaca tgtacgatca tgttcatctg cccagtcgac 50

<210> 12
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 42 bp for silencing
 expression of the PHYB gene, derived from the 5' end of PHYB
 (PHYB5hp42)-upper strand

<400> 12
 tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggagga ggccacggcc 60
 accgccacgg ccaccgccac tcccccgac tccg 94

<210> 13
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 42 bp for silencing
 expression of the PHYB gene, derived from the 5' end of PHYB
 (PHYB5hp42)-lower strand

<400> 13
 tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggcctc ctccacggcc 60
 accgccacgg ccaccgccac tcccccgac tccg 94

<210> 14
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 21 bp for silencing
 expression of the PHYB gene, derived from the 5' end of PHYB
 (PHYB5hp21)-upper strand

<400> 14
 tcgacggagt cgggggtagt ggcggaggag gccgccacta cccccgactc cg 52

<210> 15
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 21 bp for silencing
 expression of the PHYB gene, derived from the 5' end of PHYB
 (PHYB5hp21)-lower strand

<400> 15
 tcgacggagt cgggggtagt ggcggcctcc tccgccacta ccccgactc cg 52

<210> 16
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 42 bp for silencing
 expression of the PHYB gene, derived from the center of PHYB
 (PHYBChp42)-upper strand

<400> 16
 tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaacagga gggttcccc 60
 gccatatccc tacatggctg aaccacacca tcca 94

<210> 17
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 42 bp for silencing
 expression of the PHYB gene, derived from the center of PHYB
 (PHYBChp42)-lower strand

<400> 17
 tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaaccctc ctgttcccc 60
 gccatatccc tacatggctg aaccacacca tcca 94

<210> 18
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of the dsRNA encoding region of 21 bp for silencing
 expression of the PHYB gene, derived from the center of PHYB
 (PHYBChp21)-upper strand

<400> 18
tcgatggatg gtgtggttca gccataggag gatggctgaa ccacacctcc aa 52

<210> 19
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
expression of the PHYB gene, derived from the center of PHYB
(PHYBChp21)-lower strand

<400> 19
tcgatggatg gtgtggttca gccatcctcc tatggctgaa ccacaccatc ca 52

<210> 20
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
expression of the PHYB gene, derived from the 3' end of PHYB
(PHYB3hp42)-upper strand

<400> 20
tcgacattgt caactgctag tggaagtggg gacatgatgc tgatgaagga ggatcatcagc 60
atcatgtcac cacttcact agcagttgac aatg 94

<210> 21
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
expression of the PHYB gene, derived from the 3' end of PHYB
(PHYB3hp42)-lower strand

<400> 21
tcgacattgt caactgctag tggaagtggg gacatgatgc tgatgacctc ctatcatcagc 60
atcatgtcac cacttcact agcagttgac aatg 94

<210> 22
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing

expression of the PHYB gene, derived from the 3' end of PHYB
(PHYB3hp21)-upper strand

<400> 22
tcgacattgt caactgctag tggaaaggag gttccactag cagttgacaa tg 52

<210> 23
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
expression of the PHYB gene, derived from the 3' end of PHYB
(PHYB3hp21)-lower strand

<400> 23
tcgacattgt caactgctag tggaaacctcc tttccactag cagttgacaa tg 52

<210> 24
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
expression of the PDS gene (PDS42)-upper strand

<400> 24
tcgacttaac ttgtaaggaa tattacgata ctaaccgggc aatgctagga ggagcattga 60

cgggttagga tcgtaatat cttacaagt taag 94

<210> 25
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
expression of the PDS gene (PDS